0420 0590 0330 0926 0420/2220 OIPE #5

RAW SEQUENCE LISTING DATE: 10/01/2001
PATENT APPLICATION: US/09/732,436B TIME: 13:56:35

Input Set : A:\Cura-111.app
Output Set: N:\CRF3\10012001\I732436B.raw

<110> APPLICANT: Prayaga, Suhhirdas K
Shimkets, Richard A
<120> TITLE OF INVENTION: Novel Polypeptides and Polynucleotides Encoding Same
<130> FILE REFERENCE: 15966-615
<140> CURRENT APPLICATION NUMBER: 09/732,436B
<141> CURRENT FILING DATE: 2000-12-07
<150> PRIOR APPLICATION NUMBER: 60/169,887
<151> PRIOR FILING DATE: 1999-12-09
<150> PRIOR APPLICATION NUMBER: 60/170,230
<151> PRIOR FILING DATE: 1999-12-10
<160> NUMBER OF SEQ ID NOS: 26
<170> SOFTWARE: PatentIn Ver. 2.1
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<211> LENGTH: 475
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
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cagcctcttt ttacacaagg gcttgtctga tgcttggaat agggccttcc tggacaaact 180
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<213> ORGANISM: Homo sapiens
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20 25 30
Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser
35 40 45
Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His
50 55 60
Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys
65 70 75 80
Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg
85 90 95
Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn
100 105 110
Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr
115 120 125
Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn

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     72 Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu
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     79 <213> ORGANISM: Homo sapiens
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     82 <221> NAME/KEY: misc_feature
     83 <222> LOCATION: (74)..(208)
     84 <223> OTHER INFORMATION: Wherein n is a or t or c or g.
     86 <400> SEQUENCE: 3
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W--> 90 nnnnnnnnnn nnnnnnnnnn nnnnnnnnaa agctcaggtg atttctgccc tccataagat 240
     91 gcaccagcag atcttcagcc tctttttaca caagggcttg tctgatgctt ggaatagggc 300
     92 cttcctggac aaactccaga ctggatttca tcagcagctg gaagacctgg agacctgctt 360
     93 tggtatagag gatgggaagc aagagtctgc cctggaaatt gagggcccta cactggccat 420
     94 aaagaggtac ttccagggag tacatttctt cttgaaagag aggaaattca ggaactgtac 480
     95 ctgggaggtt gtcgtaatgg taaagggatt tttcttaagc acaaaacttc aagaaaaaga 540
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    101 <211> LENGTH: 199
    102 <212> TYPE: PRT
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    105 <220> FEATURE:
    106 <221> NAME/KEY: VARIANT
    107 <222> LOCATION: (24)..(68)
    108 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
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W--> 114 Ser Leu Phe Cys Asp Leu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    115              20                  25                  30
W--> 117 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    118          35                  40                  45
W--> 120 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    121      50                  55                  60
W--> 123 Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His
    124  65                  70                  75                  80
    126 Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp
    127                  85                  90                  95
    129 Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu
    130              100                 105                 110
    132 Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser
    133          115                 120                 125
    135 Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln
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139 145                 150                 155                 160
141 Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln
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144 Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys
145             180                 185                 190
147 Val Ile Tyr Leu Ala Glu Glu
148         195
151 <210> SEQ ID NO: 5
152 <211> LENGTH: 1887
153 <212> TYPE: DNA
154 <213> ORGANISM: Homo sapiens
156 <400> SEQUENCE: 5
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158 cagtcagcca cacccagccc atgtccccgc cgctgccgct gccagacaca gtcgctgccc 120
159 ctaagcgtgc tgtgcccagg ggcaggcctc ctgttcgtgc caccctcgct ggaccgccgg 180
160 gcagccgagc tgcggctggc agacaacttc atcgcctccg tgcgccgccg cgacctggcc 240
161 aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300
162 ggcgccttcg ccgacctgcg ggccctgcgt gccctgcacc tggatggcaa ccggctgacc 360
163 tcactgggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420
164 aaccagctgg cagcgctggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
165 ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggccctggg ccgcctgggc 540
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167 tcccgcctgc acaagctggc ccggctggac atgacctcca accgcctgac cacaatccca 660
168 cccgacccac tcttctcccg cctgcccctg ctcgccaggc cccggggctc gcccgcctct 720
169 gccctggtgc tggcctttgg cgggaacccc ctgcactgca actgcgagct ggtgtggctg 780
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178 gccgacactg ggcccctac cgaccgtggc gtccaggtga ctgagcacgg ggccacagct 1320
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182 gaggacagcg ccacggggct cacggccacg cggcctgtgg gctgcgcccg cttctccacc 1560
183 gaacctgcgc tgcggccatg cggggcgccg cacgctccct tcctgggcgg cacgatgatc 1620
184 atcgcgctgg gcggcgtcat cgtagcctcg gtactggtct tcatcttcgt gctgctaatg 1680
185 cgctacaagg tgcacggcgg ccagcccccc ggcaaggcca agattcccgc gcctgttagc 1740
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187 ccggagcccg cggcgctcag ggcccacacc gtggtccagc tggactgcga gccctggggg 1860
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191 <210> SEQ ID NO: 6
192 <211> LENGTH: 628
193 <212> TYPE: PRT
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Input Set : A:\Cura-111.app
Output Set: N:\CRF3\10012001\I732436B.raw

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196 <400> SEQUENCE: 6
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201 20 25 30
203 Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala
204 35 40 45
206 Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu
207 50 55 60
209 Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala
210 65 70 75 80
212 Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg
213 85 90 95
215 His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu
216 100 105 110
218 His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg
219 115 120 125
221 Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala
222 130 135 140
224 Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp
225 145 150 155 160
227 Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu
228 165 170 175
230 Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu
231 180 185 190
233 Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg
234 195 200 205
236 Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu
237 210 215 220
239 Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser
240 225 230 235 240
242 Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu
243 245 250 255
245 Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys
246 260 265 270
248 Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu
249 275 280 285
251 Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro
252 290 295 300
254 Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val
255 305 310 315 320
257 Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu
258 325 330 335
260 Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu
261 340 345 350
263 Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala
264 355 360 365
266 Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly

RAW SEQUENCE LISTING DATE: 10/01/2001
PATENT APPLICATION: US/09/732,436B TIME: 13:56:35

Input Set : A:\Cura-111.app
Output Set: N:\CRF3\10012001\I732436B.raw

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269 Pro Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro
270 385                 390                 395                 400
272 Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Pro Ser Ala Ala Ser Ala
273                 405                 410                 415
275 Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln
276             420                 425                 430
278 Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Trp Pro Asp Gln
279         435                 440                 445
281 Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser
282     450                 455                 460
284 Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser
285 465                 470                 475                 480
287 Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val
288                 485                 490                 495
290 Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro
291             500                 505                 510
293 Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly
294         515                 520                 525
296 Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly
297     530                 535                 540
299 Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met
300 545                 550                 555                 560
302 Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro
303                 565                 570                 575
305 Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro
306             580                 585                 590
308 Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala
309         595                 600                 605
311 His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu
312     610                 615                 620
314 Pro Val Gly Pro
315 625
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319 <211> LENGTH: 802
320 <212> TYPE: DNA
321 <213> ORGANISM: Equus caballus
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326 ttttccccat ggccctcctg ccctctctct tgacggccct ggtggtgtac gagttatggc 180
327 cctgtggagc tctgggctgt gacctgcctc agaaccacat cctggttagc aggaagaact 240
328 tcgtgcttct gggccaaatg agcagaatct cctccgcaat ctgtctgaag gacagaaaag 300
329 acttcaggtt cccccaggac atggcggatg gcaggcagtt cccagaggcc caggccgcgt 360
330 ctgtcctcca cgagatgctc cagcagatct tcagcctctt ccacacagag cgctcgtctg 420
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VERIFICATION SUMMARY DATE: 10/01/2001
PATENT APPLICATION: US/09/732,436B TIME: 13:56:36

Input Set : A:\Cura-111.app
Output Set: N:\CRF3\10012001\I732436B.raw

L:88 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4